```
FILE 'MEDLINE, EMBASE, BIOSIS' ENTERED AT 11:40:47 ON 31 MAY 2004
L1             0 S "FIRST SEGMENT" WITH "SECOND SEGMENT"
L2           115 S "FIRST SEGMENT" (S) "SECOND SEGMENT"
L3             6 S L2 AND "AMINO ACID"
L4             5 DUP REM L3 (1 DUPLICATE REMOVED)
L5           241 S "TRANSCRIPTION ATTENUATION"
L6          1325 S "ANTITERMINATION"
L7        952673 S "AMINO ACID"
L8        774164 S INDUCTION OR INDUCER
L9        628265 S TRANSCRIPTION
L10        48297 S STARVATION
L11           12 S L6 AND L7 AND L8 AND L9 AND L10
L12            5 DUP REM L11 (7 DUPLICATES REMOVED)
L13        48145 S OPERON
L14       267948 S TRP OR HIS
L15         1208 S L13 (S) L14
L16            1 S L15 (P) "SENSE CODON"
L17          151 S "SENSE CODON"
L18            3 S L17 (P) L6
L19            1 DUP REM L18 (2 DUPLICATES REMOVED)
L20         5357 S L7 (S) L8
L21         2352 S "RHO" (S) INDEPENDENT
L22            2 S L20 AND L21
L23            2 DUP REM L22 (0 DUPLICATES REMOVED)
L24           16 S L21 AND L6 AND L7
L25            9 DUP REM L24 (7 DUPLICATES REMOVED)

=>
```

ANSWER 1 OF 5 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 2002387746 MEDLINE
DOCUMENT NUMBER: PubMed ID: 12136084
TITLE: Transfer RNA-mediated **antitermination** in vitro.
AUTHOR: Putzer Harald; Condon Ciaran; Brechemier-Baey Dominique; Brito Renata; Grunberg-Manago Marianne
CORPORATE SOURCE: CNRS-UPR 9073, Institut de Biologie Physico-Chimique, 13 rue Pierre et Marie Curie, 75005 Paris, France.. putzer@ibpc.fr
SOURCE: Nucleic acids research, (2002 Jul 15) 30 (14) 3026-33. Journal code: 0411011. ISSN: 1362-4962.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200208
ENTRY DATE: Entered STN: 20020724
Last Updated on STN: 20020809
Entered Medline: 20020808

AB The threonyl-tRNA synthetase gene (thrS) is a member of the T-box family of approximately 250 genes, found essentially in Gram-positive bacteria, regulated by a tRNA-dependent **antitermination** mechanism in response to **starvation** for the cognate **amino acid**. While interaction between uncharged tRNA and the untranslated leader region of these genes has been firmly established by genetic means, attempts to show this interaction or to reconstitute the **antitermination** mechanism in vitro using purified tRNAs have so far failed. In addition, a number of conserved sequences have been identified in the T-box leaders, for which no function has yet been assigned. This suggests that factors other than the tRNA are important for this type of control. Here we demonstrate tRNA-mediated **antitermination** for the first time in vitro, using the regulatory tRNA(Thr) isoacceptor isolated from Bacillus subtilis and a partially purified protein fraction. As predicted by the model, aminoacylation of tRNA(Thr(GGU)) with threonine completely abolishes its ability to act as an effector. The role of the partially purified protein fraction can be functionally substituted by high concentrations of spermidine. However, this polyamine does not play a significant role in the **induction** of thrS expression in vivo, suggesting that it is specific protein co-factors that promote T-box gene regulation in conjunction with uncharged tRNA.

L12 ANSWER 2 OF 5 MEDLINE on STN DUPLICATE 2
ACCESSION NUMBER: 97252472 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9098041
TITLE: Structure and regulation of expression of the Bacillus subtilis valyl-tRNA synthetase gene.
AUTHOR: Luo D; Leautey J; Grunberg-Manago M; Putzer H
CORPORATE SOURCE: UPR 9073, CNRS, Institut de Biologie Physico-Chimique, Paris, France.
SOURCE: Journal of bacteriology, (1997 Apr) 179 (8) 2472-8. Journal code: 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X77239
ENTRY MONTH: 199705
ENTRY DATE: Entered STN: 19970523
Last Updated on STN: 19990129
Entered Medline: 19970509

AB We have sequenced the valyl-tRNA synthetase gene (valS) of Bacillus subtilis and found an open reading frame coding for a protein of 880 amino

acids with a molar mass of 101,749. The predicted **amino acid** sequence shares strong similarity with the valyl-tRNA synthetases from Bacillus stearothermophilus, Lactobacillus casei, and Escherichia coli. Extracts of B. subtilis strains overexpressing the valS gene on a plasmid have increased valyl-tRNA aminoacylation activity. Northern analysis shows that valS is cotranscribed with the folC gene (encoding folyl-polyglutamate synthetase) lying downstream. The 300-bp 5' noncoding region of the gene contains the characteristic regulatory elements, T box, "specifier codon" (GUC), and rho-independant **transcription** terminator of a gene family in gram-positive bacteria that encodes many aminoacyl-tRNA synthetases and some **amino acid** biosynthetic enzymes and that is regulated by tRNA-mediated **antitermination**. We have shown that valS expression is induced by valine limitation and that the specificity of **induction** can be switched to threonine by changing the GUC (Val) specifier triplet to ACC (Thr). Overexpression of valS from a recombinant plasmid leads to autorepression of a valS-lacZ transcriptional fusion. Like **induction** by valine **starvation**, autoregulation of valS depends on the presence of the GUC specifier codon. Disruption of the valS gene was not lethal, suggesting the existence of a second gene, as is the case for both the thrS and the tyrS genes.

L12 ANSWER 3 OF 5 MEDLINE on STN DUPLICATE 3
ACCESSION NUMBER: 96293462 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8692931
TITLE: Processing of the leader mRNA plays a major role in the **induction** of thrS expression following threonine **starvation** in Bacillus subtilis.
AUTHOR: Condon C; Putzer H; Grunberg-Manago M
CORPORATE SOURCE: Unite Propre de Recherche 9073, Institut de Biologie Physic-Chimique, Paris, France.
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1996 Jul 9) 93 (14) 6992-7. Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199608
ENTRY DATE: Entered STN: 19960911
Last Updated on STN: 19990129
Entered Medline: 19960829

AB The threonyl-tRNA synthetase gene, thrS, is a member of a family of Gram-positive genes that are induced following **starvation** for the corresponding **amino acid** by a transcriptional **antitermination** mechanism involving the cognate uncharged tRNA. Here we show that an additional level of complexity exists in the control of the thrS gene with the mapping of an mRNA processing site just upstream of the **transcription** terminator in the thrS leader region. The processed RNA is significantly more stable than the full-length transcript. Under nonstarvation conditions, or following **starvation** for an **amino acid** other than threonine, the full-length thrS mRNA is more abundant than the processed transcript. However, following **starvation** for threonine, the thrS mRNA exists primarily in its cleaved form. This can partly be attributed to an increased processing efficiency following threonine **starvation**, and partly to a further, nonspecific increase in the stability of the processed transcript under **starvation** conditions. The increased stability of the processed RNA contributes significantly to the levels of functional RNA observed under threonine **starvation** conditions, previously attributed solely to **antitermination**. Finally, we show that processing is likely to occur upstream of the terminator in the leader regions of at least four

other genes of this family, suggesting a widespread conservation of this phenomenon in their control.

L12 ANSWER 4 OF 5 MEDLINE on STN DUPLICATE 4
ACCESSION NUMBER: 96065699 MEDLINE
DOCUMENT NUMBER: PubMed ID: 7476165
TITLE: Aminoacyl-tRNA synthetase gene regulation in Bacillus subtilis: **induction**, repression and growth-rate regulation.
AUTHOR: Putzer H; Laalami S; Brakhage A A; Condon C; Grunberg-Manago M
CORPORATE SOURCE: Institut de Biologie Physico-Chimique, Paris, France.
SOURCE: Molecular microbiology, (1995 May) 16 (4) 709-18. Journal code: 8712028. ISSN: 0950-382X.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199512
ENTRY DATE: Entered STN: 19960124
Last Updated on STN: 19980206
Entered Medline: 19951214

AB The thrS gene in Bacillus subtilis is specifically induced by **starvation** for threonine and is, in addition, autorepressed by the overproduction of its own gene product, the threonyl-tRNA synthetase. Both methods of regulation employ an **antitermination** mechanism at a factor-independent **transcription** terminator that occurs just upstream of the start codon. The effector of the **induction** mechanism is thought to be the uncharged tRNA(Thr), which has been proposed to base pair in two places with the leader mRNA to induce **antitermination**. Here we show that the autoregulation by synthetase overproduction is likely to utilize a mechanism similar to that characterized for **induction** by **amino acid starvation**, that is by altering the levels of tRNA charging in the cell. We also demonstrate that the base pairing interaction at the two proposed contact points between the tRNA and the leader are necessary but not always sufficient for either form of regulation. Finally, we present evidence that the thrS gene is expressed in direct proportion to the growth rate. This method of regulation is also at the level of **antitermination** but is independent of the interaction of the tRNA with the leader region.

L12 ANSWER 5 OF 5 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
ACCESSION NUMBER: 92224133 EMBASE
DOCUMENT NUMBER: 1992224133
TITLE: Co-ordinate expression of the two threonyl-tRNA synthetase genes in Bacillus subtilis: Control by transcriptional **antitermination** involving a conserved regulatory sequence.
AUTHOR: Putzer H.; Gendron N.; Grunberg-Manago M.
CORPORATE SOURCE: CNRS, URA 1139, Ins de Biologie Physico-Chimique, 13 rue P. et M. Curie,75005 Paris, France
SOURCE: EMBO Journal, (1992) 11/8 (3117-3127). ISSN: 0261-4189 CODEN: EMJODG
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English

AB In Bacillus subtilis, two genes, thrS and thrZ, encode distinct threonyl-tRNA synthetase enzymes. Normally, only the thrS gene is expressed. Here we show that either gene, thrS or thrZ, is sufficient for

normal cell growth and sporulation. Reducing the intracellular ThrS protein concentration induces thrZ expression in a dose-compensatory manner. **Starvation** for threonine simultaneously induces thrZ and stimulates thrS expression. The 5'-leader sequences of thrS and thrZ contain, respectively, one and three **transcription** terminators preceded by a conserved sequence. We show that this sequence is essential for the regulation of thrS via a transcriptional **antitermination** mechanism. We propose that both genes, thrS and thrZ, are regulated by the same mechanism such that the additional regulatory domains present before thrZ account for its non-expression. In contrast to Escherichia coli, structurally similar regulatory domains, i.e. the consensus sequence preceeding a terminator structure, are found in the leader regions of most aminoacyl-tRNA synthetase genes of Gram-positive bacteria. This suggests that they are regulated by a common mechanism.

=>

ANSWER 1 OF 2 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
on STN

ACCESSION NUMBER: 91267371 EMBASE
DOCUMENT NUMBER: 1991267371
TITLE: Transcriptional attenuation control of ermK, a macrolide-lincosamide-streptogramin B resistance determinant from Bacillus licheniformis.
AUTHOR: Kwak J.-H.; Choi E.-C.; Weisblum B.
CORPORATE SOURCE: Department of Pharmacology, University of Wisconsin, Medical School,Madison, WI 53706, United States
SOURCE: Journal of Bacteriology, (1991) 173/15 (4725-4735).
ISSN: 0021-9193 CODEN: JOBAAY
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
037 Drug Literature Index
LANGUAGE: English
SUMMARY LANGUAGE: English

AB ermK instructs bacteria to synthesize an erythromycin-inducible 23S rRNA methylase that confers resistance to the macrolide, lincosamide, and streptogramin B antibiotics. Expression of ermK is regulated by transcriptional attenuation, in contrast to other inducible erm genes, previously described, which are regulated translationally. The ermK mRNA leader sequence has a total length of 357 nucleotides and encodes a 14-**amino-acid** leader peptide together with its ribosome binding site. Additionally, the mRNA leader sequence can fold in either of two mutually exclusive conformations, one of which is postulated to form in the absence of **induction** and to contain two **rho** factor-**independent** terminators. Truncated transcription products ca. 210 and 333 nucleotides long were synthesized in the absence of **induction**, both in vivo and in vitro, as predicted by the transcriptional attenuation model; run-off transcription in vitro with rITP favored the synthesis of the full-length run-off transcript over that of the 210- and 333-nucleotide truncated products. Northern (RNA) blot analysis of transcripts synthesized in vivo in the absence of erythromycin indicated that transcription terminated at either of the two inverted complementary repeat sequences in the leader that were postulated to serve as **rho** factor-**independent** terminators; moreover, no full-length transcripts were detectable in the uninduced samples. In contrast, full-length (ca. 1,200-nucleotide) transcripts were only detected in RNA samples synthesized in vivo in the presence of erythromycin. Full-length transcripts formed in the absence of **induction** from transcriptional readthrough past the two proposed transcription terminators would fold in a way that would sequester the ribosome binding site together with the first two codons of the ErmK methylase, reducing its efficiency in translation. This feature could therefore provide additional control of expression in the absence of **induction**; however, such regulation, if operative, would act only secondarily, both in time and place, relative to transcriptional control. Analysis by reverse transcriptase mapping of in vivo transcripts from two primers that bracket the transcription terminator responsible for the 210-nucleotide truncated fragment supports the transcriptional attenuation model proposed and suggests further that the synthesis of the ermK message is initiated constitutively upstream of the proposed terminator but completed inductively downstream of this site.

L23 ANSWER 2 OF 2 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
on STN

ACCESSION NUMBER: 90054679 EMBASE
DOCUMENT NUMBER: 1990054679
TITLE: Nucleotide sequences of the Erwinia chrysanthemi ogl and pelE genes negatively regulated by the kdgR gene product.
AUTHOR: Reverchon S.; Huang Y.; Bourson C.; Robert-Baudouy J.

CORPORATE SOURCE: Lab. de Genetique Moleculaire, des Microorganismes, Inst. Nat. Sci. Appliquees, 20 Avenue Albert Einstein,69621 Villeurbanne, France
SOURCE: Gene, (1989) 85/1 (125-134).
ISSN: 0378-1119 CODEN: GENED6
COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
022 Human Genetics
LANGUAGE: English
SUMMARY LANGUAGE: English
AB The nucleotide sequences of the coding and regulatory regions of the genes encoding oligogalacturonate lyase (OGL) and pectate lyase e isoenzyme (PLe) from Erwinia chrysanthemi 3937 were determined. The ogl sequence contains an open reading frame (ORF) of 1164 bp coding for a 388-**amino acid** (aa) polypeptide with a predicted M(r) of 44124. A possible transcriptional start signal showing homology with the Escherichia coli promoter consensus sequence was detected. In addition, a sequence 3' to the coding region was found to be able to form a secondary structure which may function as an **Rho-independent** transcriptional termination signal. For the pelE sequence, a long ORF of 1212 bp coding for a 404-aa polypeptide was detected. PLe is secreted into the external medium by E. chrysanthemi, and a potential signal peptide sequence was identified in the pelE gene. In the 5' upstream pelE coding region, a putative promoter resembling E. coli promoter consensus sequences was detected. Furthermore, the region immediately 3' to the pelE translational stop codon may function as an **Rho-independent** translational termination signal. In strain 3937, the synthesis of OGL and PLe, as well as the other enzymes involved in the pectin-degradative pathway (particularly the kdgT product), are known to be regulated by the KdgR repressor, which mediates galacturonate and polygalacturonate **induction**. Synthesis of these enzymes is also regulated by the CRP-cAMP complex which mediates catabolite repression. Analysis of the regulatory regions of ogl and pelE allowed us to identify possible CRP-binding sites for these two genes. Furthermore, comparative study of the regulatory regions of the ogl, kdgT and pelE genes revealed the existence of a highly conserved sequence which could correspond to a whole or partial KdgR-binding site.

=>